



CRF Problem Report

The Scientific and Technical Information Center (STIC) experienced a problem when processing the following computer readable form (CRF):

Application Serial Number: 09/841,720C
Filing Date: 4-24-2001
Date Processed by STIC: 6-14-02

STIC Contact: Mark Spencer, 703-308-4212

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JUL 08 2002

TECH CENTER 1600/2900

Nature of Problem:

The CRF (was):

- ☒ (circle one) Damaged or Unreadable (for Unreadable, see attached)
☐ Blank (no files on CRF) (see attached)
☐ Empty file (filename present, but no bytes in file) (see attached)
☐ Virus-infected. Virus name: _____ The STIC will not process the CRF.
☐ Not saved in ASCII text
☐ Sequence Listing was embedded in the file. According to Sequence Rules, submitted file should **only** be the Sequence Listing.
☐ Did not contain a Sequence Listing. (see attached sample)
☐ Other: _____

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1. EFS-Bio (<<http://www.uspto.gov/ebs/efs/downloads/documents.htm>> , EFS Submission User Manual - ePAVE)
2. U.S. Postal Service: U.S. Patent and Trademark Office, Box Sequence, P.O. Box 2327, Arlington, VA 22202
3. Hand Carry directly to:
U.S. Patent and Trademark Office, Technology Center 1600, Reception Area, 7th Floor, Examiner Name, Sequence Information, Crystal Mall One, 1911 South Clark Street, Arlington, VA 22202
Or
U.S. Patent and Trademark Office, Box Sequence, Customer Window, Lobby, Room 1B03, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202
4. Federal Express, United Parcel Service , or other delivery service to: U.S. Patent and Trademark Office, Box Sequence, Room 1B03-Mailroom, Crystal Plaza Two, 2011 South Clark Place, Arlington, VA 22202

Revised 01/29/2002

0590

10/09

OIPE

RAW SEQUENCE LISTING

DATE: 06/14/2001

PATENT APPLICATION: US/09/841,720

TIME: 15:43:26

Input Set : N:\Crf3\RULE60\09841720.txt

Output Set: N:\CRF3\06142001\I841720.raw

SEQUENCE LISTING

3 (1) GENERAL INFORMATION:

5 (i) APPLICANT: Yu, Lei

7 (ii) TITLE OF INVENTION: MU OPIOID RECEPTORS: COMPOSITIONS AND
8 METHODS

10 (iii) NUMBER OF SEQUENCES: 9

12 (iv) CORRESPONDENCE ADDRESS:

13 (A) ADDRESSEE: Arnold, White & Durkee

14 (B) STREET: P.O. Box 4433

15 (C) CITY: Houston

16 (D) STATE: Texas

17 (E) COUNTRY: USA

18 (F) ZIP: 77210

20 (v) COMPUTER READABLE FORM:

21 (A) MEDIUM TYPE: Floppy disk

22 (B) COMPUTER: IBM PC compatible

23 (C) OPERATING SYSTEM: PC-DOS/MS-DOS

24 (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

26 (vi) CURRENT APPLICATION DATA:

C--> 27 (A) APPLICATION NUMBER: US/09/841,720

C--> 28 (B) FILING DATE: 24-Apr-2001

29 (C) CLASSIFICATION:

31 (vii) PRIOR APPLICATION DATA:

32 (A) APPLICATION NUMBER: 08/120,601

33 (B) FILING DATE: 13-SEP-1993

36 (viii) ATTORNEY/AGENT INFORMATION:

37 (A) NAME: Wilson, Mark B.

38 (B) REGISTRATION NUMBER: 37,259

39 (C) REFERENCE/DOCKET NUMBER: INDA:002

41 (ix) TELECOMMUNICATION INFORMATION:

42 (A) TELEPHONE: 512/418-3000

43 (B) TELEFAX: 512/474-7577

46 (2) INFORMATION FOR SEQ ID NO: 1:

48 (i) SEQUENCE CHARACTERISTICS:

49 (A) LENGTH: 1618 base pairs

50 (B) TYPE: nucleic acid

51 (C) STRANDEDNESS: single

52 (D) TOPOLOGY: linear

55 (ix) FEATURE:

56 (A) NAME/KEY: CDS

57 (B) LOCATION: 214..1407

60 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

62 CGTGGAAGGG GGCTACAAGC AGAGGAGAAT ATCAGACGCT CAGACGTTCC CTTCTGCCTG 60

64 CCGCTCTTCT CTGGTTCCAC TAGGGCTGGT CCATGTAAGA ATCTGACGGA GCCTAGGGCA 120

66 GCTGTGAGAG GAAGAGGCTG GGGCGCGTGG AACCCGAAAA GTCTGAGTGC TCTCAGTTAC 180

68 AGCCTACCTA GTCCGCAGCA GGCCTTCAGC ACC ATG GAC AGC AGC ACC GGC CCA 234

69 Met Asp Ser Ser Thr Gly Pro

ENTERED

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Input Set : N:\Cr3\RULE60\09841720.txt

Output Set: N:\CRF3\06142001\I841720.raw

70									1				5				
72	GGG	AAC	ACC	AGC	GAC	TGC	TCA	GAC	CCC	TTA	GCT	CAG	GCA	AGT	TGC	TCC	282
73	Gly	Asn	Thr	Ser	Asp	Cys	Ser	Asp	Pro	Leu	Ala	Gln	Ala	Ser	Cys	Ser	
74			10						15				20				
76	CCA	GCA	CCT	GGC	TCC	TGG	CTC	AAC	TTG	TCC	CAC	GTT	GAT	GGC	AAC	CAG	330
77	Pro	Ala	Pro	Gly	Ser	Trp	Leu	Asn	Leu	Ser	His	Val	Asp	Gly	Asn	Gln	
78			25					30				35					
80	TCC	GAT	CCA	TGC	GGT	CTG	AAC	CGC	ACC	GGG	CTT	GGC	GGG	AAC	GAC	AGC	378
81	Ser	Asp	Pro	Cys	Gly	Leu	Asn	Arg	Thr	Gly	Leu	Gly	Gly	Asn	Asp	Ser	
82	40					45				50					55		
84	CTG	TGC	CCT	CAG	ACC	GGC	AGC	CCT	TCC	ATG	GTC	ACA	GCC	ATT	ACC	ATC	426
85	Leu	Cys	Pro	Gln	Thr	Gly	Ser	Pro	Ser	Met	Val	Thr	Ala	Ile	Thr	Ile	
86				60					65				70				
88	ATG	GCC	CTC	TAC	TCT	ATC	GTG	TGT	GTA	GTG	GGC	CTC	TTC	GGA	AAC	TTC	474
89	Met	Ala	Leu	Tyr	Ser	Ile	Val	Cys	Val	Val	Gly	Leu	Phe	Gly	Asn	Phe	
90				75				80				85					
92	CTG	GTC	ATG	TAT	GTG	ATT	GTA	AGA	TAC	ACC	AAA	ATG	AAG	ACT	GCC	ACC	522
93	Leu	Val	Met	Tyr	Val	Ile	Val	Arg	Tyr	Thr	Lys	Met	Lys	Thr	Ala	Thr	
94			90				95				100						
96	AAC	ATC	TAC	ATT	TTC	AAC	CTT	GCT	CTG	GCA	GAC	GCC	TTA	GCG	ACC	AGT	570
97	Asn	Ile	Tyr	Ile	Phe	Asn	Leu	Ala	Leu	Ala	Asp	Ala	Leu	Ala	Thr	Ser	
98		105				110			115								
100	ACA	CTG	CCC	TTT	CAG	AGT	GTC	AAC	TAC	CTG	ATG	GGA	ACA	TGG	CCC	TTC	618
101	Thr	Leu	Pro	Phe	Gln	Ser	Val	Asn	Tyr	Leu	Met	Gly	Thr	Trp	Pro	Phe	
102	120				125				130						135		
104	GGA	ACC	ATC	CTC	TGC	AAG	ATC	GTG	ATC	TCA	ATA	GAT	TAC	TAC	AAC	ATG	666
105	Gly	Thr	Ile	Leu	Cys	Lys	Ile	Val	Ile	Ser	Ile	Asp	Tyr	Tyr	Asn	Met	
106				140				145				150					
108	TTC	ACC	AGC	ATA	TTC	ACC	CTC	TGC	ACC	ATG	AGC	GTG	GAC	CGC	TAC	ATT	714
109	Phe	Thr	Ser	Ile	Phe	Thr	Leu	Cys	Thr	Met	Ser	Val	Asp	Arg	Tyr	Ile	
110			155				160				165						
112	GCT	GTC	TGC	CAC	CCA	GTC	AAA	GCC	CTG	GAT	TTC	CGT	ACC	CCC	CGA	AAT	762
113	Ala	Val	Cys	His	Pro	Val	Lys	Ala	Leu	Asp	Phe	Arg	Thr	Pro	Arg	Asn	
114			170				175				180						
116	GCC	AAA	ATC	GTC	AAC	GTC	TGC	AAC	TGG	ATC	CTC	TCT	TCT	GCC	ATC	GGT	810
117	Ala	Lys	Ile	Val	Asn	Val	Cys	Asn	Trp	Ile	Leu	Ser	Ser	Ala	Ile	Gly	
118		185				190			195								
120	CTG	CCT	GTA	ATG	TTC	ATG	GCA	ACC	ACA	AAA	TAC	AGG	CAG	GGG	TCC	ATA	858
121	Leu	Pro	Val	Met	Phe	Met	Ala	Thr	Thr	Lys	Tyr	Arg	Gln	Gly	Ser	Ile	
122	200				205				210						215		
124	GAT	TGC	ACC	CTC	ACG	TTC	TCC	CAC	CCA	ACC	TGG	TAC	TGG	GAG	AAC	CTG	906
125	Asp	Cys	Thr	Leu	Thr	Phe	Ser	His	Pro	Thr	Trp	Tyr	Trp	Glu	Asn	Leu	
126				220				225				230					
128	CTC	AAA	ATC	TGT	GTC	TTT	ATC	TTC	GCT	TTC	ATC	ATG	CCG	ATC	CTC	ATC	954
129	Leu	Lys	Ile	Cys	Val	Phe	Ile	Phe	Ala	Phe	Ile	Met	Pro	Ile	Leu	Ile	
130			235				240				245						
132	ATC	ACT	GTG	TGT	TAC	GGC	CTG	ATG	ATC	TTA	CGA	CTC	AAG	AGC	GTT	CGC	1002
133	Ile	Thr	Val	Cys	Tyr	Gly	Leu	Met	Ile	Leu	Arg	Leu	Lys	Ser	Val	Arg	
134			250				255				260						

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TIME: 15:43:26

Input Set : N:\Crf3\RULE60\09841720.txt

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136 ATG CTA TCG GGC TCC AAA GAA AAG GAC AGG AAT CTG CGC AGG ATC ACC      1050
137 Met Leu Ser Gly Ser Lys Glu Lys Asp Arg Asn Leu Arg Arg Ile Thr
138      265      270      275
140 CGG ATG GTG CTG GTG GTC GTG GCT GTA TTT ATC GTC TGC TGG ACC CCC      1098
141 Arg Met Val Leu Val Val Ala Val Phe Ile Val Cys Trp Thr Pro
142 280      285      290      295
144 ATC CAC ATC TAC GTC ATC ATC AAA GCG CTG ATC ACG ATT CCA GAA ACC      1146
145 Ile His Ile Tyr Val Ile Ile Lys Ala Leu Ile Thr Ile Pro Glu Thr
146      300      305      310
148 ACA TTT CAG ACC GTT TCC TGG CAC TTC TGC ATT GCT TTG GGT TAC ACG      1194
149 Thr Phe Gln Thr Val Ser Trp His Phe Cys Ile Ala Leu Gly Tyr Thr
150      315      320      325
152 AAC AGC TGC CTG AAT CCA GTT CTT TAC GCC TTC CTG GAT GAA AAC TTC      1242
153 Asn Ser Cys Leu Asn Pro Val Leu Tyr Ala Phe Leu Asp Glu Asn Phe
154      330      335      340
156 AAG CGA TGC TTC AGA GAG TTC TGC ATC CCA ACC TCG TCC ACG ATC GAA      1290
157 Lys Arg Cys Phe Arg Glu Phe Cys Ile Pro Thr Ser Ser Thr Ile Glu
158      345      350      355
160 CAG CAA AAC TCC ACT CGA GTC CGT CAG AAC ACT AGG GAA CAT CCC TCC      1338
161 Gln Gln Asn Ser Thr Arg Val Arg Gln Asn Thr Arg Glu His Pro Ser
162 360      365      370      375
164 ACG GCT AAT ACA GTG GAT CGA ACT AAC CAC CAG CTA GAA AAT CTG GAG      1386
165 Thr Ala Asn Thr Val Asp Arg Thr Asn His Gln Leu Glu Asn Leu Glu
166      380      385      390
168 GCA GAA ACT GCT CCA TTG CCC TAACTGGGTC TCACACCATC CAGACCCTCG      1437
169 Ala Glu Thr Ala Pro Leu Pro
170      395
172 CTAAGCTTAG AGGCCGCCAT CTACGTGGAA TCAGGTTGCT GTCAGGGTGT GTGGGAGGCT      1497
174 CTGGTTTCCT GAGAAACCAT CTGATCCTGC ATTCAAAGTC ATTCCTCTCT GGCTACTTCA      1557
176 CTCTGCACAT GAGAGATGCT CAGACTGATC AAGACCAGAA GAAAGAAGAG ACTACCGGAC      1617
178 A      1618
181 (2) INFORMATION FOR SEQ ID NO: 2:
183 (i) SEQUENCE CHARACTERISTICS:
184 (A) LENGTH: 398 amino acids
185 (B) TYPE: amino acid
186 (D) TOPOLOGY: linear
188 (ii) MOLECULE TYPE: protein
190 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:
192 Met Asp Ser Ser Thr Gly Pro Gly Asn Thr Ser Asp Cys Ser Asp Pro
193 1      5      10      15
195 Leu Ala Gln Ala Ser Cys Ser Pro Ala Pro Gly Ser Trp Leu Asn Leu
196      20      25      30
198 Ser His Val Asp Gly Asn Gln Ser Asp Pro Cys Gly Leu Asn Arg Thr
199      35      40      45
201 Gly Leu Gly Gly Asn Asp Ser Leu Cys Pro Gln Thr Gly Ser Pro Ser
202      50      55      60
204 Met Val Thr Ala Ile Thr Ile Met Ala Leu Tyr Ser Ile Val Cys Val
205      65      70      75      80
207 Val Gly Leu Phe Gly Asn Phe Leu Val Met Tyr Val Ile Val Arg Tyr

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208          85          90          95
210 Thr Lys Met Lys Thr Ala Thr Asn Ile Tyr Ile Phe Asn Leu Ala Leu
211          100          105          110
213 Ala Asp Ala Leu Ala Thr Ser Thr Leu Pro Phe Gln Ser Val Asn Tyr
214          115          120          125
216 Leu Met Gly Thr Trp Pro Phe Gly Thr Ile Leu Cys Lys Ile Val Ile
217          130          135          140
219 Ser Ile Asp Tyr Tyr Asn Met Phe Thr Ser Ile Phe Thr Leu Cys Thr
220 145          150          155          160
222 Met Ser Val Asp Arg Tyr Ile Ala Val Cys His Pro Val Lys Ala Leu
223          165          170          175
225 Asp Phe Arg Thr Pro Arg Asn Ala Lys Ile Val Asn Val Cys Asn Trp
226          180          185          190
228 Ile Leu Ser Ser Ala Ile Gly Leu Pro Val Met Phe Met Ala Thr Thr
229          195          200          205
231 Lys Tyr Arg Gln Gly Ser Ile Asp Cys Thr Leu Thr Phe Ser His Pro
232          210          215          220
234 Thr Trp Tyr Trp Glu Asn Leu Leu Lys Ile Cys Val Phe Ile Phe Ala
235 225          230          235          240
237 Phe Ile Met Pro Ile Leu Ile Ile Thr Val Cys Tyr Gly Leu Met Ile
238          245          250          255
240 Leu Arg Leu Lys Ser Val Arg Met Leu Ser Gly Ser Lys Glu Lys Asp
241          260          265          270
243 Arg Asn Leu Arg Arg Ile Thr Arg Met Val Leu Val Val Val Ala Val
244          275          280          285
246 Phe Ile Val Cys Trp Thr Pro Ile His Ile Tyr Val Ile Ile Lys Ala
247          290          295          300
249 Leu Ile Thr Ile Pro Glu Thr Thr Phe Gln Thr Val Ser Trp His Phe
250 305          310          315          320
252 Cys Ile Ala Leu Gly Tyr Thr Asn Ser Cys Leu Asn Pro Val Leu Tyr
253          325          330          335
255 Ala Phe Leu Asp Glu Asn Phe Lys Arg Cys Phe Arg Glu Phe Cys Ile
256          340          345          350
258 Pro Thr Ser Ser Thr Ile Glu Gln Gln Asn Ser Thr Arg Val Arg Gln
259          355          360          365
261 Asn Thr Arg Glu His Pro Ser Thr Ala Asn Thr Val Asp Arg Thr Asn
262          370          375          380
264 His Gln Leu Glu Asn Leu Glu Ala Glu Thr Ala Pro Leu Pro
265 385          390          395

```

268 (2) INFORMATION FOR SEQ ID NO: 3:

270 (i) SEQUENCE CHARACTERISTICS:

271 (A) LENGTH: 1618 base pairs

272 (B) TYPE: nucleic acid

273 (C) STRANDEDNESS: single

274 (D) TOPOLOGY: linear

277 (ix) FEATURE:

278 (A) NAME/KEY: CDS

279 (B) LOCATION: 339..1232

282 (xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

RAW SEQUENCE LISTING

DATE: 06/14/2001

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TIME: 15:43:26

Input Set : N:\Crf3\RULE60\09841720.txt

Output Set: N:\CRF3\06142001\I841720.raw

```

284 CGTGGGAAGGG GGCTACAAGC AGAGGAGAAT ATCAGACGCT CAGACGTTCC CTTCTGCCTG      60
286 CCGCTCTTCT CTGGTTCAC TAGGGCTGGT CCATGTAAGA ATCTGACGGA GCCTAGGGCA      120
288 GCTGTGAGAG GAAGAGGCTG GGGCGCGTGG AACCCGAAAA GTCTGAGTGC TCTCAGTTAC      180
290 AGCCTACCTA GTCCGCAGCA GGCCTTCAGC ACCATGGACA GCAGCACCGG CCCAGGGAAC      240
292 ACCAGCGACT GCTCAGACCC CTTAGCTCAG GCAAGTTGCT CCCCAGCACC TGGCTCCTGG      300
294 CTCAACTTGT CCCACGTTGA TGGCAACCAG TCCGATCC ATG CGG TCT GAA CCG      353
295                                     Met Arg Ser Glu Pro
296                                     1                               5
298 CAC CGG GCT TGG CGG GAA CGA CAG CCT GTG CCC TCA GAC CGG CAG CCC      401
299 His Arg Ala Trp Arg Glu Arg Gln Pro Val Pro Ser Asp Arg Gln Pro
300                                     10                               20
302 TTC CAT GGT CAC AGC CAT TAC CAT CAT GGC CCT CTA CTC TAT CGT GTG      449
303 Phe His Gly His Ser His Tyr His His Gly Pro Leu Leu Tyr Arg Val
304                                     25                               30                               35
306 TGT AGT GGG CCT CTT CGG AAA CTT CCT GGT CAT GTA TGT GAT TGT AAG      497
307 Cys Ser Gly Pro Leu Arg Lys Leu Pro Gly His Val Cys Asp Cys Lys
308                                     40                               45                               50
310 ATA CAC CAA AAT GAA GAC TGC CAC CAA CAT CTA CAT TTT CAA CCT TGC      545
311 Ile His Gln Asn Glu Asp Cys His Gln His Leu His Phe Gln Pro Cys
312                                     55                               60                               65
314 TCT GGC AGA CGC CTT AGC GAC CAG TAC ACT GCC CTT TCA GAG TGT CAA      593
315 Ser Gly Arg Arg Leu Ser Asp Gln Tyr Thr Ala Leu Ser Glu Cys Gln
316                                     70                               75                               80                               85
318 CTA CCT GAT GGG AAC ATG GCC CTT CGG AAC CAT CCT CTG CAA GAT CGT      641
319 Leu Pro Asp Gly Asn Met Ala Leu Arg Asn His Pro Leu Gln Asp Arg
320                                     90                               95                               100
322 GAT CTC AAT AGA TTA CTA CAA CAT GTT CAC CAG CAT ATT CAC CCT CTG      689
323 Asp Leu Asn Arg Leu Leu Gln His Val His Gln His Ile His Pro Leu
324                                     105                               110                               115
326 CAC CAT GAG CGT GGA CCG CTA CAT TGC TGT CTG CCA CCC AGT CAA AGC      737
327 His His Glu Arg Gly Pro Leu His Cys Cys Leu Pro Pro Ser Gln Ser
328                                     120                               125                               130
330 CCT GGA TTT CCG TAC CCC CCG AAA TGC CAA AAT CGT CAA CGT CTG CAA      785
331 Pro Gly Rhe Pro Tyr Pro Pro Lys Cys Gln Asn Arg Gln Arg Leu Gln
332                                     135                               140                               145
334 CTG GAT CCT CTC TTC TGC CAT CGG TCT GCC TGT AAT GTT CAT GGC AAC      833
335 Leu Asp Pro Leu Phe Cys His Arg Ser Ala Cys Asn Val His Gly Asn
336                                     150                               155                               160                               165
338 CAC AAA ATA CAG GCA GGG GTC CAT AGA TTG CAC CCT CAC GTT CTC CCA      881
339 His Lys Ile Gln Ala Gly Val His Arg Leu His Pro His Val Leu Pro
340                                     170                               175                               180
342 CCC AAC CTG GTA CTG GGA GAA CCT GCT CAA AAT CTG TGT CTT TAT CTT      929
343 Pro Asn Leu Val Leu Gly Glu Pro Ala Gln Asn Leu Cys Leu Tyr Leu
344                                     185                               190                               195
346 CGC TTT CAT CAT GCC GAT CCT CAT CAT CAC TGT GTG TTA CGG CCT GAT      977
347 Arg Phe His His Ala Asp Pro His His His Cys Val Leu Arg Pro Asp
348                                     200                               205                               210
350 GAT CTT ACG ACT CAA GAG CGT TCG CAT GCT ATC GGG CTC CAA AGA AAA      1025
351 Asp Leu Thr Thr Gln Glu Arg Ser His Ala Ile Gly Leu Gln Arg Lys

```

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/841,720

DATE: 06/14/2001

TIME: 15:43:27

Input Set : N:\Crf3\RULE60\09841720.txt

Output Set: N:\CRF3\06142001\I841720.raw

L:27 M:220 C: Keyword misspelled or invalid format, [(A) APPLICATION NUMBER:]

L:28 M:220 C: Keyword misspelled or invalid format, [(B) FILING DATE:]